

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of the claims in the application.

Listing of Claims:

1. (Currently Amended) A method for searching for a ~~specific~~ base sequence, in genes with an apparatus comprising the step of:

~~an acquisition step for a specific base sequence candidate, which acquires a specific base sequence candidate, which is a candidate of a specific base sequence appearing in a base sequence of an expressed gene;~~

~~a searching step for a specific base sequence, which searches a matching base sequence, which is a base sequence matching the specific base sequence candidate acquired by said acquisition step for specific base sequence candidate, from a set of base sequences, which include a union of sets of~~

~~a union of sets of exon base sequences, and~~

~~a set of border base sequences, which straddle exon borders in the expressed gene formed by a plurality of exons; and~~

~~a determination step, which determines whether the specific base sequence candidate acquired by said acquisition step for a specific base sequence candidate is a specific base sequence based on whether a plurality of matching base sequences are included in the search result by said search step for a specific base sequence~~ allowing the apparatus to search for the base sequence in base sequences consisting of: base sequences in each of exons of the genes, and base sequences straddling exon borders in each of the genes having a plurality of exons.

2. (Currently Amended)      ~~The method for searching for a specific base sequence according to claim 1, wherein~~

~~attribute information including information indicating the position of exon sequence, or information for identifying gene formed by exon, is correlated to an element of said union of set of exon~~  
each of the base sequences consisting of the base sequences in each of exons of the genes and the base sequences straddling exon borders in each of the genes having a plurality of exons, the attribute information including information indicating the position of the exons in the genome sequence or information for identifying the genes.

3. (Currently Amended)      ~~The method for searching for a specific base sequence according to claim 1, wherein~~

~~said set of border in the case that the base sequences straddling exon borders are overlapping, the overlapping sequences are integrated is acquired based on a set acquired by integrating information indicating a base sequence, which has same expressed gene and overlapping position of base sequence, to the set of information, which indicates a base sequence straddling the exon border in the expressed gene formed by a plurality of exons, and indicates the base sequence of the same length as that of the base sequence of said specific base sequence candidate.~~

4. (Currently Amended)      ~~The method for searching for a specific base sequence according to claim 1, comprising: an acquisition step for allowable number of matches, which acquires a numerical value, indicating the number of allowable mismatching bases, as a degree of matching between the base sequence included in said set of base sequences and the base sequence indicated by said specific base sequence candidate, wherein said searching step for~~

~~the base sequence carries out search based on the allowable number of matches acquired by said acquisition step for allowable number of matches~~ is searched with at least one mismatch allowed.

5. (Currently Amended)      ~~The method for searching for a specific base sequence according to claim~~  
 [[4]] 1, further comprising:

~~an acquisition step for mismatching base pair, which acquires a base pair, which is determined to be mismatching by said searching step for base sequence~~ the step of allowing the apparatus to determine whether the base sequence appears only in the target gene, based on whether a plurality of base sequences are identified.

Claims 6 - 9      Cancelled

10. (Currently Amended)      An apparatus for searching for a specific base sequence, comprising:

~~a storage for storing set of base sequences, which stores a set of base sequences in each of exons of the genes, which includes a union of sets of~~

~~a union of sets of exon base sequences; and~~

~~a set of border base sequences, which straddles straddling exon border borders in each of the expressed gene formed by genes having a plurality of exons;~~

~~an acquirer for specific base sequence candidate, which acquires a specific base sequence candidate, which is a candidate of a specific base sequence appearing in a base sequence of an expressed gene; and~~

~~a searcher for specific base sequence, which searches searching for a matching base sequence, which is a base sequence matching the specific base sequence candidate acquired by said acquirer for~~

~~specific base sequence candidate, from the base sequences included in the set of base sequences stored~~  
~~[[by]] in said storage for set of base sequences.~~

11. (Currently Amended)      The apparatus ~~for searching for specific base sequence~~ according to claim 10, wherein

~~attribute information, including information indicating position of exon sequence, or information for identifying gene formed by exon, is correlated [[with]] to an element of said union of sets of exon each~~  
of the base sequences consisting of the base sequences in each of exons of the genes and the base sequences straddling exon borders in each of the genes having a plurality of exons, the attribute information including information indicating the position of the exons in the genome sequence or information for identifying the genes.

12. (Currently Amended)      The apparatus ~~for searching for a specific base sequence~~ according to claim 10, wherein

~~said set of border in the case that the base sequences is acquired based on a set acquired by integrating information indicating a base sequence, which has the same expressed gene and overlapping position of base sequence, as the set of information, which indicates a base sequence straddling the exon border in the expressed gene formed by a plurality of exons, and indicates the base sequence of the same length as that of the base sequence of said specific base sequence candidate~~ straddling exon borders are overlapping, the overlapping sequences are integrated.

13. (Currently Amended)      The apparatus ~~for searching for specific base sequence~~ according to claim 10, ~~comprising: an acquirer for allowable number of matches, which acquires a numerical value, indicating~~

~~the number of allowable mismatching bases, as a degree of matching between the base sequence included in said set of base sequences and the base sequence indicated by said specific base sequence candidate, wherein said searcher for wherein~~

~~the base sequence carries out search based on the allowable number of matches acquired by said acquirer for allowable number of matches is searched with at least one mismatch allowed.~~

Claims 14 - 16 Cancelled

17. (Withdrawn) An apparatus for storing set of base sequences, storing a set of base sequences including a union of sets of exon base sequences, and a set of border base sequences straddling exon border in the expressed gene formed by a plurality of exons, in a searchable state.

18. (Withdrawn) The apparatus for storing a set of base sequences according to claim 17, wherein attribute information, including information indicating position of exon sequence, or information for identifying gene formed by exon, is correlated to an element of said union of sets of exon base sequences.

19. (Withdrawn) The storage for set of base sequence according to claim 17, wherein said set of border base sequences is acquired based on a set acquired by integrating information indicating a base sequence, which has the same expressed gene and overlapping position of base sequence, to the set of information, which indicates a base sequence straddling the exon border in the expressed gene formed by a plurality of exons, and indicates the base sequence of the same length as that of the base sequence as an input for searching.

20. (Withdrawn)        A generation method for set of base sequence, comprising: an acquisition step for length of base sequence candidate, which acquires length of specific base sequence candidate appearing in a base sequence of an expressed gene; an acquisition step for set of exon base sequences, which acquires a union of sets of exon base sequences; a generation step for set of border base sequences, which generates a set of base sequences by integrating information indicating a base sequence, which has the same expressed gene and overlapping position of base sequence, to the set of information, which indicates a base sequence straddling the exon border in the expressed gene formed by a plurality of exons, and indicates the base sequence of the same length as that acquired by said acquisition step for length of base sequence candidate; and a generation step for union of sets, which generates a union of sets of the base sequences acquired by said acquisition step for set of exon base sequences, and set of the base sequences generated by said generation step for set of border base sequences.

21. (Cancelled)

22. (Withdrawn)        A generation program for a specific base sequence, causing a computer to carry out: an acquisition step for length of base sequence candidate, which acquires length of specific base sequence candidate appearing in a base sequence of an expressed gene; an acquisition step for set of exon base sequences, which acquires a union of sets of exon base sequences; a generation step for set of border base sequences, which generates a set of base sequence by integrating information indicating a base sequence, which has same expressed gene and overlapping position of base sequence, to the set of information, which indicates a base sequence straddling the exon border in the expressed gene formed by a plurality of exons, and indicates the base sequence of the same length as that acquired by said acquisition step for length of base sequence candidate; and a generation step for union of sets, which generates a union



of set of the base sequences acquired by said acquisition step for set of exon base sequences, and set of the base sequences generated by said generation step for set of border base sequences

Claims 23 – 24 Cancelled

25. (Withdrawn)        The storage for set of base sequence according to claim 18, wherein said set of border base sequences is acquired based on a set acquired by integrating information indicating a base sequence, which has the same expressed gene and overlapping position of base sequence, to the set of information, which indicates a base sequence straddling the exon border in the expressed gene formed by a plurality of exons, and indicates the base sequence of the same length as that of the base sequence as an input for searching.

26. (Cancelled)